

Alfalfa benefits from *Medicago truncatula*: The RCT1 gene from *M. truncatula* confers broad-spectrum resistance to anthracnose in alfalfa

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Alfalfa is economically the most important forage legume worldwide. A recurrent challenge to alfalfa production is the significant yield loss caused by disease. Although knowledge of molecular mechanisms underlying host resistance should facilitate the genetic improvement of alfalfa, the acquisition of such knowledge is hampered by alfalfa's tetrasomic inheritance and outcrossing nature. However, alfalfa is congeneric with the reference legume *Medicago truncatula*, providing an opportunity to use *M. truncatula* as a surrogate to clone the counterparts of many agronomically important genes in alfalfa. In particular, the high degree of sequence identity and remarkably conserved genome structure and function between the two species enables *M. truncatula* genes to be used directly in alfalfa improvement. We report the map-based cloning of RCT1, a host resistance (R) gene in *M. truncatula* that confers resistance to multiple races of *Colletotrichum trifolii*, a hemibiotrophic fungal pathogen that causes anthracnose disease of alfalfa. RCT1 is a member of the Toll-interleukin-1 receptor/nucleotide-binding site/leucine-rich repeat (TIR-NBS-LRR) class of plant R genes and confers broad-spectrum anthracnose resistance when transferred into susceptible alfalfa plants. Thus, RCT1 provides a novel resource to develop anthracnose-resistant alfalfa cultivars and contributes to our understanding of host resistance against the fungal genus *Colletotrichum*. This work demonstrates the potential of using *M. truncatula* genes for genetic improvement of alfalfa.